SEQUENCE LISTING

<110> Sakowicz, Roman
      Goldstein, Lawrence S. B.
      The Regents of the University of California

<120> Identification and Expression of a Novel Kinesin Motor
      Protein

<130> 18557C-000710US

<140> US 09/235,416
<141> 1999-01-22

<150> WO PCT/US99/01355
<151> 1999-01-22

<150> US 60/072,361
<151> 1998-01-23

<160> 7

<170> PatentIn Ver. 2.0

<210> 1
<211> 784
<212> PRT
<213> Thermomyces lanuginosus

<220>
<223> TL-gamma ATP-dependent plus end-directed
      microtubule motor protein

<220>
<221> DOMAIN
<222> (1)..(357)
<223> kinesin-like microtubule motor domain

<220>
<221> DOMAIN
<222> (358)..(442)
<223> neck domain links motor domain to stalk domain

<220>
<221> DOMAIN
<222> (443)..(601)
<223> stalk domain, unc-104 family domain

<220>
<221> DOMAIN
<222> (602)..(784)
<223> tail domain

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<221> VARIANT
<222> (713)
<223> polymorphic variant #1 Val -> Ile

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<221> VARIANT
<222> (762)
<223> polymorphic variant #2 Asp -> Glu

<220>
<221> VARIANT
<222> (774)
<223> polymorphic variant #3 Glu -> Asp

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             20                  25                  30

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             35                  40                  45

Arg Lys Ser Gly Lys Thr Ile Met Asp Gly Pro Lys Ala Phe Ala Phe
     50                  55                  60

Asp Arg Ser Tyr Trp Ser Phe Asp Lys Asn Ala Pro Asn Tyr Ala Arg
65                  70                  75                      80

Gln Glu Asp Leu Phe Gln Asp Leu Gly Val Pro Leu Leu Asp Asn Ala
             85                  90                      95

Phe Lys Gly Tyr Asn Asn Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser
             100                 105                 110

Gly Lys Ser Tyr Ser Met Met Gly Tyr Gly Lys Glu His Gly Val Ile
         115                 120                 125

Pro Arg Ile Cys Gln Asp Met Phe Arg Arg Ile Asn Glu Leu Gln Lys
     130                 135                 140

Asp Lys Asn Leu Thr Cys Thr Val Glu Val Ser Tyr Leu Glu Ile Tyr
145                 150                 155                 160

Asn Glu Arg Val Arg Asp Leu Leu Asn Pro Ser Thr Lys Gly Asn Leu
             165                 170                 175

Lys Val Arg Glu His Pro Ser Thr Gly Pro Tyr Val Glu Asp Leu Ala
             180                 185                 190

Lys Leu Val Val Arg Ser Phe Gln Glu Ile Glu Asn Leu Met Asp Glu
         195                 200                 205

Gly Asn Lys Ala Arg Thr Val Ala Ala Thr Asn Met Asn Glu Thr Ser
     210                 215                 220

Ser Arg Ser His Ala Val Phe Thr Leu Thr Leu Thr Gln Lys Trp His
225                 230                 235                 240

Asp Glu Glu Thr Lys Met Asp Thr Glu Lys Val Ala Lys Ile Ser Leu
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Val Asp Leu Ala Gly Ser Glu Arg Ala Thr Ser Thr Gly Ala Thr Gly
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Ala Arg Leu Lys Glu Gly Ala Glu Ile Asn Arg Ser Leu Ser Thr Leu
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Gly Arg Val Ile Ala Ala Leu Ala Asp Met Ser Ser Gly Lys Gln Lys
    290           295           300

Lys Asn Gln Leu Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu
305           310           315           320

Lys Asp Ser Leu Gly Gly Asn Ser Met Thr Ala Met Ile Ala Ala Ile
            325           330           335

Ser Pro Ala Asp Ile Asn Phe Glu Glu Thr Leu Ser Thr Leu Arg Tyr
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Ala Asp Ser Ala Lys Arg Ile Lys Asn His Ala Val Val Asn Glu Asp
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Pro Asn Ala Arg Met Ile Arg Glu Leu Lys Glu Glu Leu Ala Gln Leu
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Arg Ser Lys Leu Gln Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Gly
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Ser Gly Gly Pro Val Glu Glu Ser Tyr Pro Pro Asp Thr Pro Leu Glu
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Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met
            420           425           430

Ser Lys Ala Glu Ile Val Glu Gln Leu Asn Gln Ser Glu Lys Leu Tyr
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Arg Asp Leu Asn Gln Thr Trp Glu Glu Lys Leu Ala Lys Thr Glu Glu
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Ile His Lys Glu Arg Glu Ala Ala Leu Glu Glu Leu Gly Ile Ser Ile
465           470           475           480

Glu Lys Gly Phe Val Gly Pro Tyr His Ser Lys Glu Met Pro His Leu
            485           490           495

Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn
            500           505           510

Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln
    515           520           525

Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr
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Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala
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Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg
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Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn
            580           585           590
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Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe
            645             650             655

Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys
        660             665             670

Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val
        675             680             685

Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp
        690             695             700

Ser Asp Ser Gln Ser Ser Phe Pro Val Arg Asp Lys Tyr Met Ser Asn
705             710             715             720

Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly
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Thr Pro Arg Ser Asp Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys
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Lys Ser Lys Gln Asp Ala Ser Asn Val Asp Val Glu Glu Leu Arg Gln
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<210> 2
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<212> DNA
<213> Thermomyces lanuginosus

<220>
<223> TL-gamma ATP-dependent plus end-directed
      microtubule motor protein

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cctccgggtg ccgaagagaa ggcgcgtaaa agtggcaaaa ctattatgga tggcccgaag 180
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caggaagacc tattccaaga tctcggagtc ccgcttctgg ataatgcatt caaggggttat 300
aacaattgta tcttcgccta cggtcagacc ggttcgggca agtcctattc aatgatgggc 360
tatggcaagg agcatggcgt gatcccgcgg atttgccagg acatgttccg gcgtattaat 420
gaactgcaga aggacaagaa cctcacttgc accgtcgaag tttcgtactt ggaaatttac 480
aatgaacgag tgcgagagtt gctgaatccg tcgacaaagg ggaatctcaa ggtccgagaa 540
cacccgtcga ccggcccgta cgtggaggac ttggcgaagc tggtcgtgcg atcattccaa 600
gaaatcgaaa atctcatgga tgagggcaac aaagccagaa cggttgccgc cacaaacatg 660
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ggaaaacaga agaagaatca gttagtacct taccgagatt cggtactgac gtggcttctg 960
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<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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<210> 4
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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gaattcctgc ttcgctgttt tca                                           23

<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate
      forward primer
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A'
concl'd.

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<220>
<221> modified_base
<222> (25)
<223> n = a, c, g or t


<400> 5
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<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence:degenerate
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<221> modified_base
<222> (16)
<223> n = a, c, g or t


<220>
<221> modified_base
<222> (28)
<223> n = a, c, g or t


<400> 6
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<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence:degenerate
      reverse primer


<220>
<221> modified_base
<222> (16)
<223> n = a, c, g or t


<220>
<221> modified_base
<222> (28)
<223> n = a, c, g or t


<400> 7
gcgcgaattc tcdctnccdg cvarrtcnac                                    30
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